



MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTGVQR  
PCRRDSPTTCGCPCCRHTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF  
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA  
LNVPGSSSHDTLCTSTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE  
GWGPTPRAGRAALQLKLRRLTELLGAQDGALLVRLQLRVARMPLERSVRERFLPVH

### FIG. 1

TCCGCAGGC GGACC GGGGGCAAAGGAGGTGGCATGTCGGTCAGGCACAGCAGGGT CCTGT  
GTCCCGC CTGAGCC CGCTCTCCCTGCTCCAGCAAGGACC  
><Met {trans=1-s, dir=f, res=1}>  
ATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGCCCTGGTGTGGCGCTGCCTGCC  
CTGCTGCCGGTGC CGCTGTACCGGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC  
GCAGAGACAGGGGAGCGGGCTGGTGTGCGCCAGTGC CCCCCCAGGCACCTTGTGCAGCGG  
CCGTGCCGCCAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCCACTACACGAG  
TTCTGGA ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCCTCTGCCGGGAGCGTGAGGAG  
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGACCGGCTCTTC  
GCGCACGCTGGTTCTGCTTGAGCACGCATCGTGTCCACCTGGTGC CGGTGATTGCC  
CCGGCACCCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCGGGAGGCACCTCTCAGCC  
AGCAGCTCCAGCTCAGAGCAGTGC CAGCCCACCGCAACTGCACGCCCTGGCCTGGCC  
CTCAATGTGCCAGGCTTCCCTCCATGACACCCCTGTGCACCAGCTGCACTGGCTTCCC  
CTCAGCACCAAGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTATCGACTTGTGGCT  
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGAG  
GGCTGGGGTCCGACACCAAGGGCGGGCGCGCGGCCCTTGCA GCTGAAGCTGCGTCCGG  
CTCACGGAGCTCCTGGGGCGCAGGACGGGGCGCTGCTGGTGC GGCTGCTGCAGGGCTG  
CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCCTGCAC  
TGATCCTGGCCCCCTTATTATTCATCCTGGCACCCACTGCACTGAAAGAGG  
CTTTTTTAAATAAGAAGAAATGAGGTTNTTAAAAAAAAAAAAAAA

### FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCCACTACACG  
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCCTGNGG  
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCAACCGTGCCT  
GCCGCTGCCGCACCGCTTCTCGCGCACGCTGGTTCTGCTGGAGCAC  
GCATCGTGTCCACCTGGTGC CGCTGATTGCCCGGGCACCCCCAGCCA  
GAACACGCAGTGCCTAGCGTGCCCCCAGGCACCTCTCAGCCAGCAGC  
TCCAGCTCAGAGCAGTGC CAGCCCCACCGCAACTGCACGCCCTGGCCT  
GCCCTCAATGTGCCAGGCTTCCCTCCATGACACCCCTGTGCACCAGCT  
GCACTGGCTTCCCTCAGCACCAAGGGTACCAGGAGCTGAGGAGTGTGAG  
CGTGCCTGTCATCGACTTGTGGCTTCCAGGACATCTCCAT

### FIG. 3



SEQ ID NO:4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCAGGCCACTACACG  
 SEQ ID NO:5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCAGGCCACTACACG  
 SEQ ID NO:6 1 G  
 SEQ ID NO:3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCAGGCCACTACACG  
  
 SEQ ID NO:4 178 CA-TTCTGGAACTACCTGGAGCGC  
 SEQ ID NO:5 51 CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCCTGNNG  
 SEQ ID NO:6 2 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCCTGCGG  
 SEQ ID NO:3 51 CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCCTGNNG  
  
 SEQ ID NO:5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCAACCGCGCCT  
 SEQ ID NO:6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCAACCGTGCGCT  
 SEQ ID NO:7 1 GAGGGGGCCCCCAGGAGTGGTGGCCGGAGGTG  
 SEQ ID NO:3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCAACCGTGCGCT  
  
 SEQ ID NO:5 151 GCNGCTGCAGCACCGGNTTCTCGCGCACGCTGNTTCTGCTTGGAGCAC  
 SEQ ID NO:6 102 GCCGCTGCCGCACCCGGCTTCTCGCGCACGCTGGTTCTGCTTGGAGCAC  
 SEQ ID NO:7 32 TGGCAGGGGTCAAGGTTGCTGGTCCCAGCCTTGCACCCCTGAGCTAGGACAC  
 SEQ ID NO:3 151 GCCGCTGCCGCACCCGGCTTCTCGCGCACGCTGGTTCTGCTTGGAGCAC  
  
 SEQ ID NO:5 201 GCATCGTGTCCACCTGGTGNCGCGTGATTGCNCGGGCACCCCCAGCCA  
 SEQ ID NO:6 152 GCATCGTGTCCACCTGGTGCACGGCGTGATTNCCCCGGGCACCCCCAGCCA  
 SEQ ID NO:7 82 CAGTTCCCCCTGACCCCTGTTCTCCCTCCTGGCTGCAGGGACCCCCAGCCA  
 SEQ ID NO:8 1 GCATCGTGTCCACCTGGTGCACGGCGTGATTGCCCGGGCACCCCCAGCCA  
 SEQ ID NO:10 1 CTTGTCCACCTGGTGCACGGCGTGATTNCCC-GGGCACCCCCAGCCA  
 SEQ ID NO:3 201 GCATCGTGTCCACCTGGTGCACGGCGTGATTGCCCGGGCACCCCCAGCCA  
  
 SEQ ID NO:5 251 GAACACGCA-TGCAAAGCCGTG  
 SEQ ID NO:7 132 GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCAGCCAGCAGC  
 SEQ ID NO:8 51 GAACACGCAAG-CCTAGCCGTGCCCCCAGGCACCTTCAGCCAGCAGC  
 SEQ ID NO:10 47 GAACACGCAAGTGCC-AGCCNT-CCCCCAGGCACCTTCAGCCAGCAGC  
 SEQ ID NO:9 1 AGCNGTGCNCNCAGGCACCTTCAGCCAGCAGT  
 SEQ ID NO:3 251 GAACACGCAAGTGCCTAGCCGTGCCCCCAGGCACCTTCAGCCAGCAGC  
  
 SEQ ID NO:7 182 TCCAGCTCAGAGCAGTGCACAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
 SEQ ID NO:8 101 TCCAGCTCAGAGCAGTGCACAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
 SEQ ID NO:10 97 TCCAGCTCAGAGCAGTGCACAGCCCCACCGCAACTGCAACGCCCTGGNC-T  
 SEQ ID NO:9 36 TCCAGCTCAGAGCAGTGCACAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
 SEQ ID NO:3 301 TCCAGCTCAGAGCAGTGCACAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
  
 SEQ ID NO:7 232 GGCCCTCAATGTGCCAGGCTTCCCTCCATGACACCCCTGTGCACCAAG  
 SEQ ID NO:8 151 GGCCCTCAATGTGCCAGGCTTCCCTCCATGACACCCCTGTGCACCAAGCT  
 SEQ ID NO:10 147 GGCCCTCAATGTGCCAGGCTTCCCTCCATGACACCCCTGTGCACCAAGCT  
 SEQ ID NO:9 86 GGCCCTCAATGTGCCAGGCTTCCCTCCATGACACGCTGTGCACCAAGCT  
 SEQ ID NO:3 351 GGCCCTCAATGTGCCAGGCTTCCCTCCATGACACCCCTGTGCACCAAGCT  
  
 SEQ ID NO:10 197 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAAGGAGCTGAGGAGTGTGAG  
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 SEQ ID NO:10 247 CGTGCCGTACCGACTTTGTGGCTTCCAGGACATCTCCAT  
 SEQ ID NO:9 186 CGTGCCGTACCGACTTTGTGGCTTCCAGGACATCTCCAT  
 SEQ ID NO:3 451 CGTGCCGTACCGACTTTGTGGCTTCCAGGACATCTCCAT

# FIG. 4



DNA30942 1 M R A L E G P G L S L C L V L A L P A L L P V P A V R G V A E T P T Y P W R D . A E T G  
htNFR2 1 M A P V A V W A A L C L V L E L W A A A H A L P A Q V A F T P V . A P E P G S T C R L R E Y Y D Q T

DNA30942 45 E R L V C A Q C P P G T F V Q R P C R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V L  
htNFR2 50 A Q M C C S K C S P G Q H A K V F C T K T S D T V C D S C E D S T Y T Q I W N W V P E C L S C G S R

DNA30942 95 C G E R E E E A R A C H A T H N R A C R C R T G F F . . . A H A G . . . F C L E H A S C P P G A C V  
htNFR2 100 C S S D Q V E T Q A C T R E Q N R I C T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G F G V

DNA30942 139 I A P G T P S Q N T Q C Q P C P P G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S S S  
htNFR2 150 A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C R P H Q I C N V V A . . . I P G N A S

DNA30942 189 H D T L C T S C T G F P L S T R V P G A E E C E R A V I D F V A F Q D I S I K R L Q R L L Q A L E A  
htNFR2 196 R D A V C T S . . P T R S M A P G A V H L P Q P V S T R S Q H T Q P T P E P S T A P S T S F L L

DNA30942 239 P E G W G P T P . . R A G R A A L Q L K L R R R L T E L L G A Q D G A L L V R L L Q A L R V A R M P  
htNFR2 244 P M G P S P P A E G S T G D F A L P V G L I V G V T A L G L L I T I V N C V I M T Q V K K P L

DNA30942 287 G L E R S V R E R F L P V H  
htNFR2 293 C L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S S L E S S A S A L D R R A

htNFR2 343 P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C I V N V C S S S D

htNFR2 393 H S S Q C S S Q A S S T M G D T D S S P S E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G

FIG. 5



DcR3 1 M R A [ E G P G L S L E C E V L A L P A L L P V F A V R G V A 31  
OPG 1 M N K L L C C A L V F L D L S I K W T T Q E T F P - - - - 25

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62  
OPG 26 - - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93  
OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD1

CRD2

DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124  
OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3

CRD4

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P P 155  
OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD3

CRD4

DcR3 156 G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S 186  
OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L T Q K G N 178

DcR3 187 S S H D T L C T G F P L S T R V P G A E E C E R A V I D 217  
OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247  
OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L R R R L T E L L G A Q D G A L - L V R L L 277  
OPG 240 I K R Q H S S Q E Q T F Q L L K W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300  
OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

FIG. 6

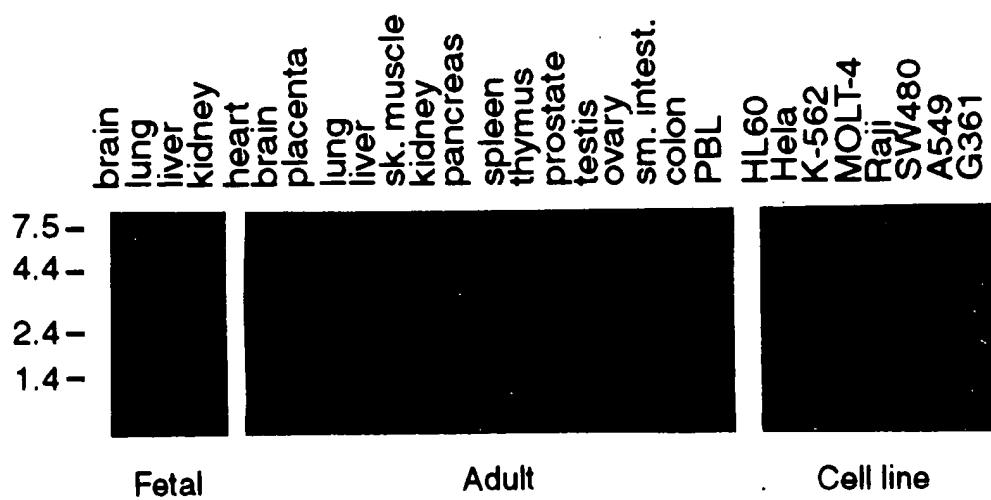
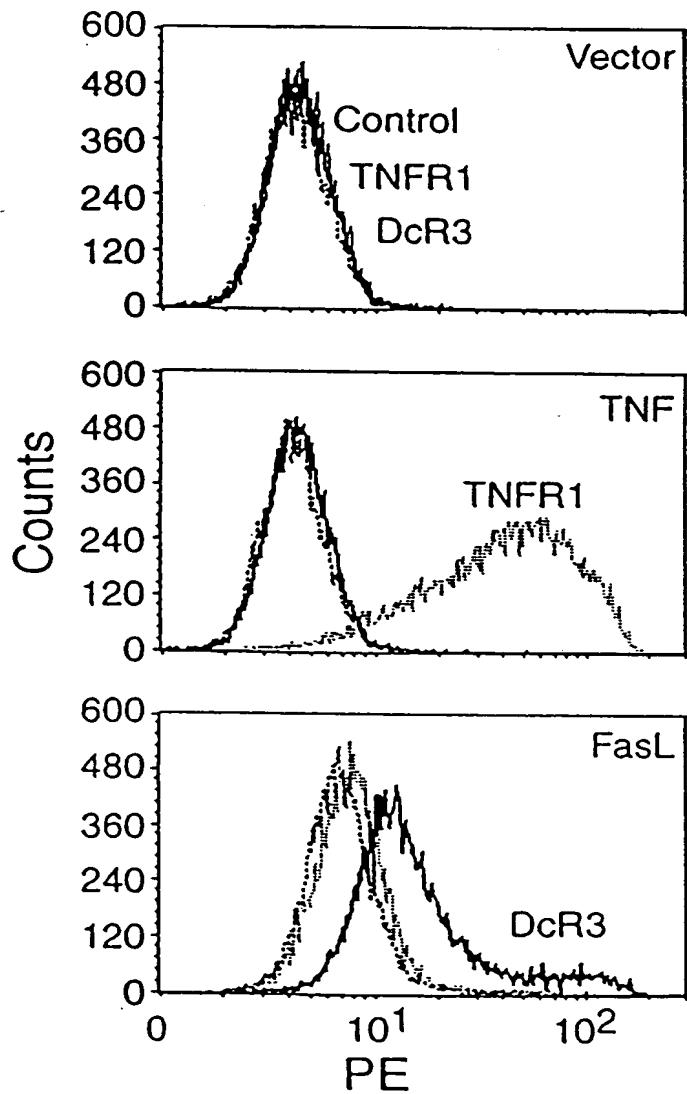
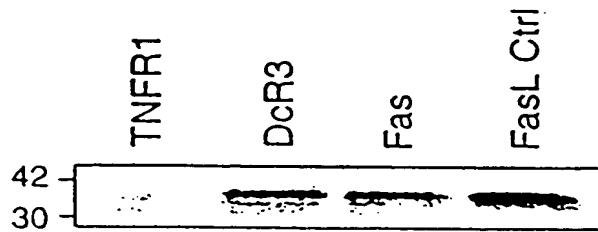


FIG. 7



**FIG. 8A**



**FIG. 8B**

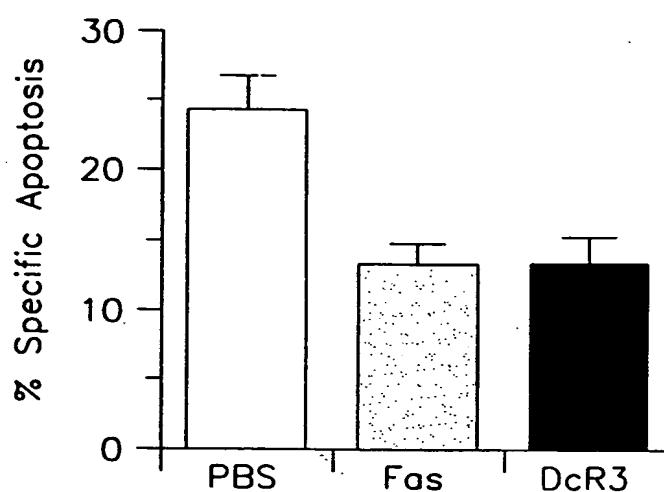


FIG. 9A

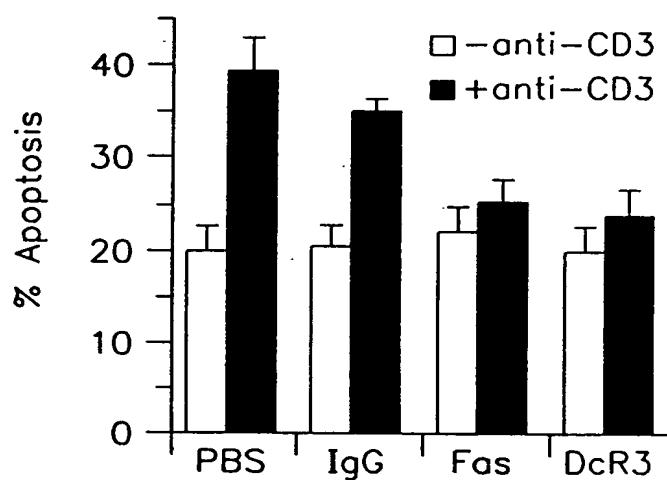


FIG. 9B

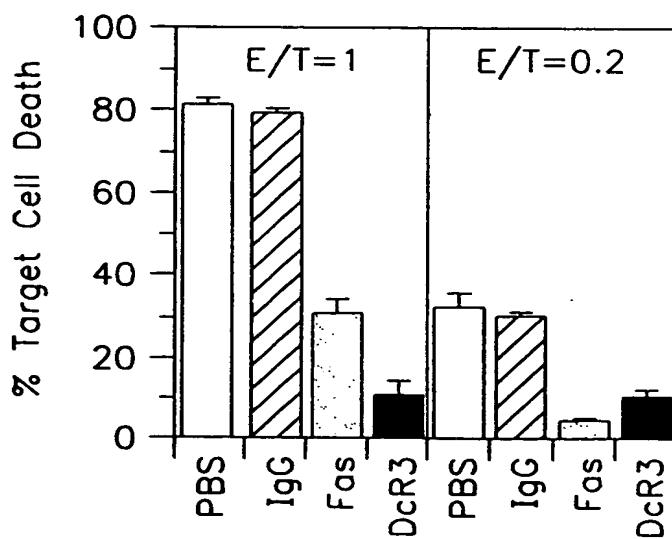
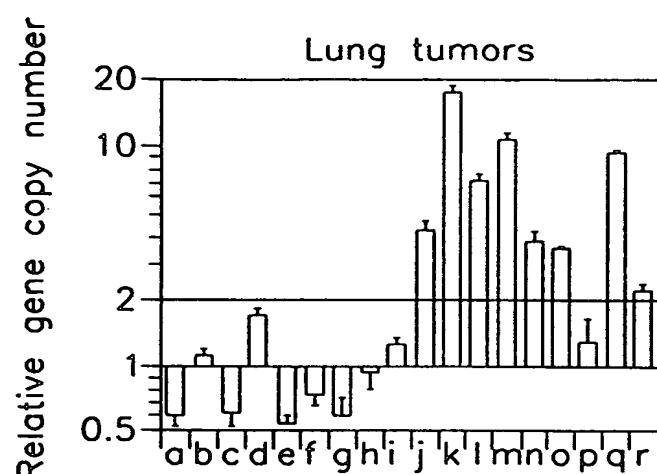
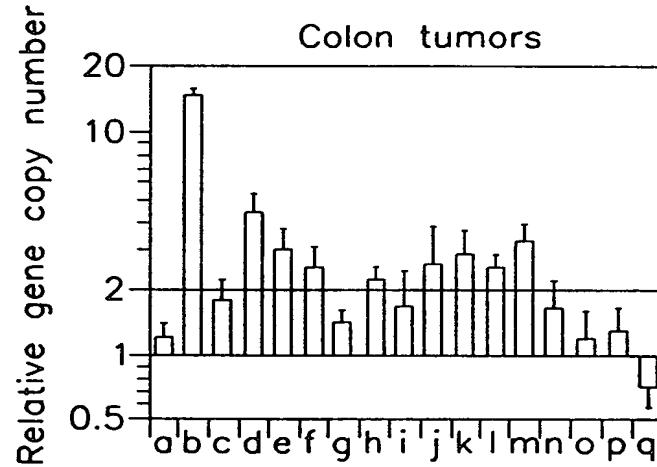
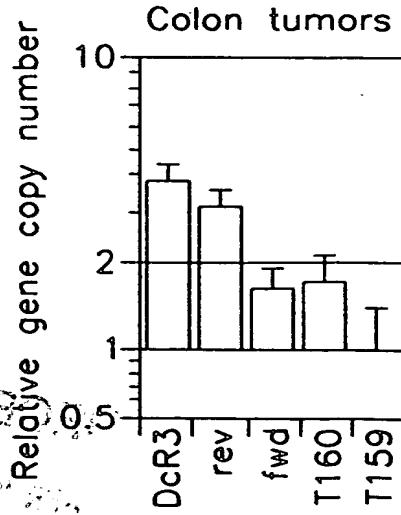
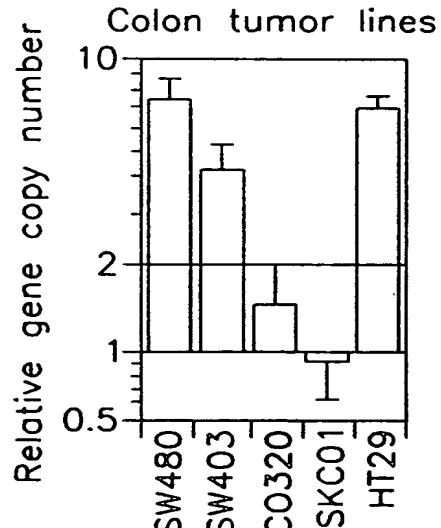


FIG. 9C

**FIG. IOA****FIG. IOB****FIG. IOC****FIG. IOD**

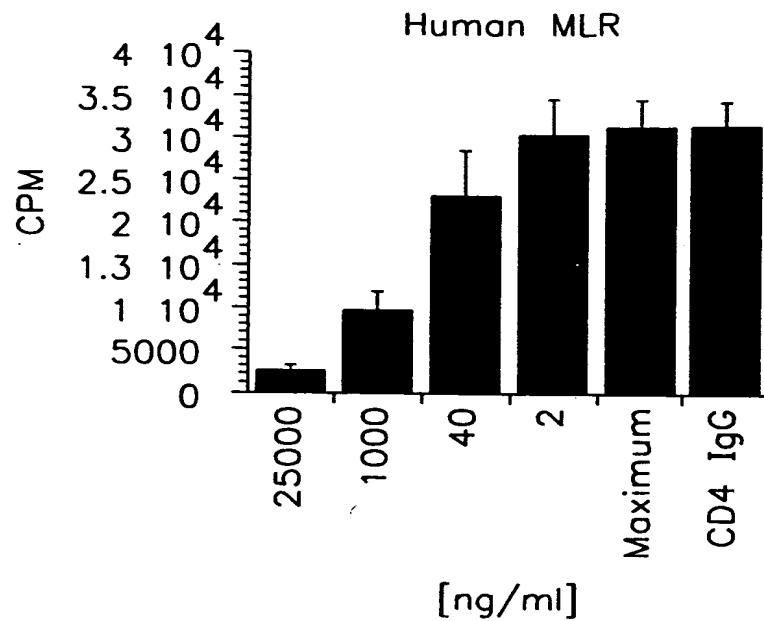


FIG. I IA

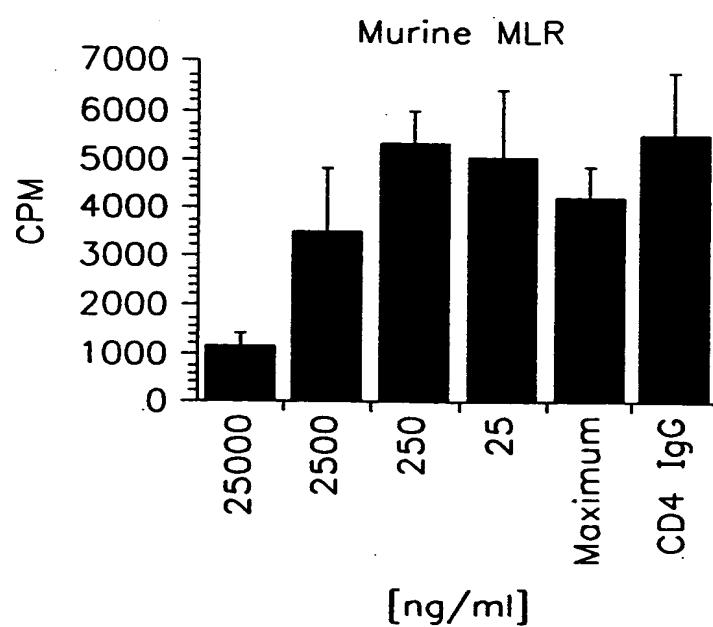


FIG. I IB

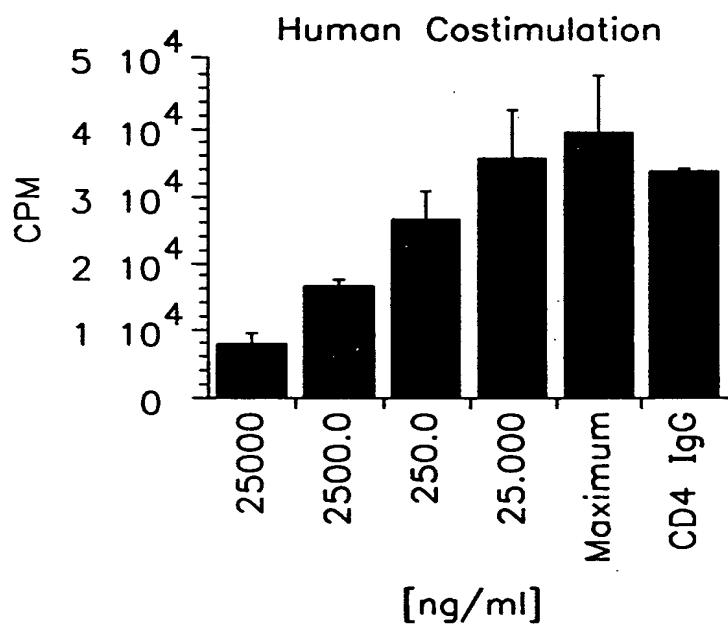


FIG. 1 IC



mAb	Isotype	Antigen Specificity (ELISA)				% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1 OPG	
4B7.1.1	IgG1	+++	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.  
% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

FIG. 12

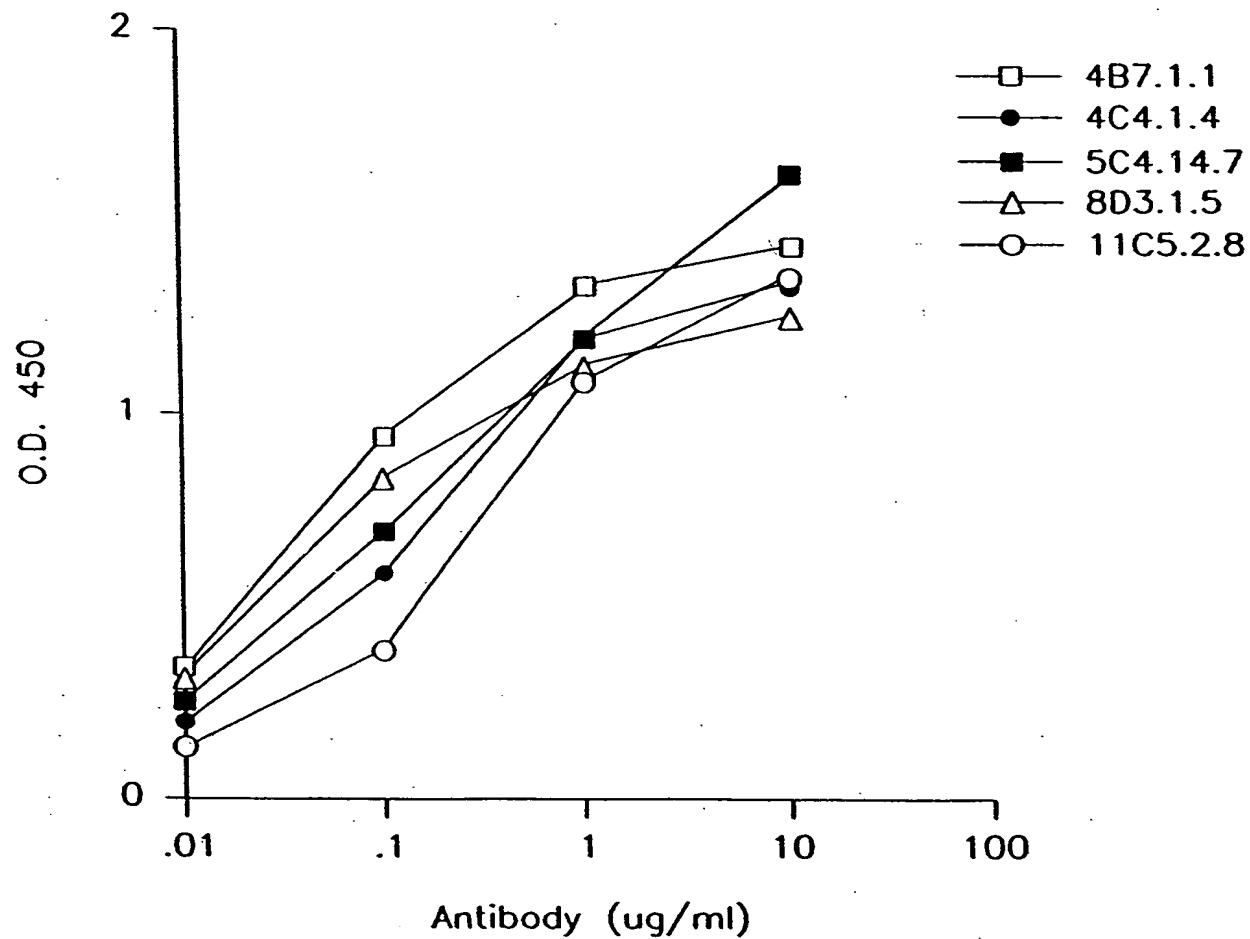


FIG. 13

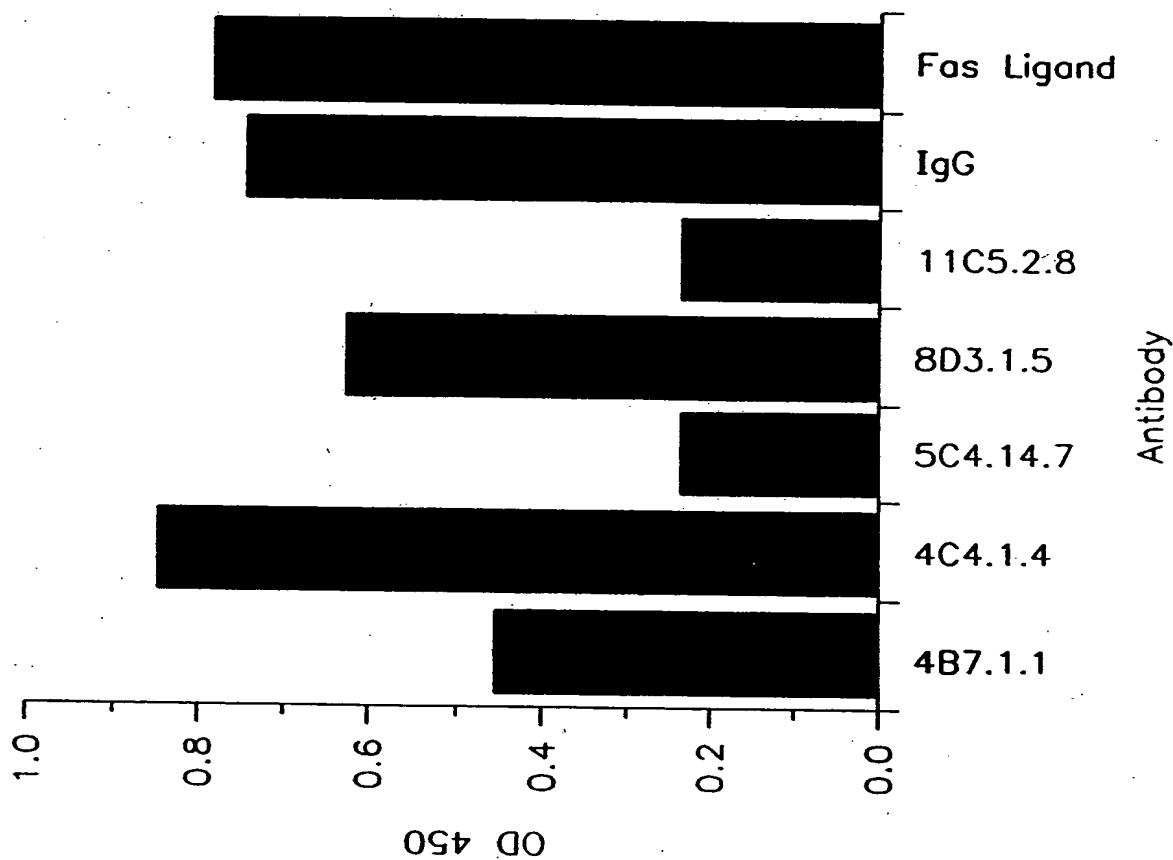


FIG. 14